

1 **Ten Simple Rules on How to Organise a Bioinformatics**

2 **Hackathon**

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21 **Abstract**

22 The completion of the human genome sequence triggered world-wide efforts to unravel the secrets
23 sequestered in its deceptively simple code. Numerous bioinformatics projects were undertaken to
24 hunt for genes, to predict their protein products, their functions and post-translational modifications,
25 to analyse protein-protein interactions, etc. In their wake, these diverse projects produced many novel
26 analytic and predictive computer programs, fully optimised for manipulating human genome
27 sequence data. The EU-funded project AllBio “Broadening the Bioinformatics Infrastructure to
28 unicellular, animal and plant science” (FP7 GA 289452), concentrated on non-human genomes,
29 applying human-genome-derived computational solutions to non-human genomics research
30 questions. After several events for community building to get an overview about state-of-the-art of
31 the bioinformatics in the non-human bioinformatics life science areas, the AllBio partners collected
32 “test cases” to identify gaps and existing challenges in the bioinformatics field from the user
33 communities. Form the collected test cases, 14 were selected encompassing unicellular organisms,
34 plants and farm animals to be addressed in so-called “hackathons”. A hackathon is an event in which
35 bioinformatics developers convene to work together to produce new software tools and webservice
36 as solutions to the challenges provided. These hackathons have been extremely successful and
37 produced not only new software solutions, but also provided an excellent basis to integrate existing
38 knowledge, to join “wet lab” and “dry lab” experts, to provide hands-on training in bioinformatics, and
39 enforce cross disciplinary interaction. The scientific communities could promote and implement
40 hackathons as a routine activity e.g. in the educational system or for PhD students in the life sciences.
41 Encouraging interdisciplinary interaction in the hackathons could leverage the existing resources and
42 avoid duplication of efforts. The consortium developed 10 Rules as recommendations how to organise
43 hackathons in the life sciences based on the experience in AllBio to make the information available to
44 the life science communities.

45 **Introduction**

46 The completion of the human genome sequence triggered world-wide efforts to unravel the secrets
47 sequestered in its deceptively simple code. Numerous bioinformatics projects were undertaken to

48 hunt for genes, to predict their protein products, their functions and post-translational modifications,
49 to analyse protein-protein interactions, etc. In their wake, these diverse projects produced many novel
50 analytic and predictive computer programs, fully optimised for manipulating human genome
51 sequence data.

52 This focus on exploring the human genome is understandable – we are inevitably anthropocentric. In
53 consequence, considerably less effort has been invested in exploring the many thousands of other
54 available genomes, from unicellular organisms to plants and non-human animals, a detailed
55 understanding of which is, nevertheless, likely to have significant impact on human health and well-
56 being. Nevertheless, recent advances in genome sequencing technology, informatics, automation,
57 artificial intelligence, etc. have allowed us to extend the reach of genomic research to all organisms.
58 Among other large-scale sequencing initiatives for plants, microbes or animals like fish, the Earth
59 Biogenome Project (EBP) [1] was launched with the aim of sequencing the DNA of all life on earth
60 within the next decade. This long-term project will lead both to a greater understanding of Earth's
61 biodiversity and to responsible stewardship of its resources, tackling the most crucial scientific and
62 social challenges of the new millennium. While the focus of the EBP is on the collection of genomic
63 data, other initiatives have centred on data analysis. The EU-funded project AllBio "Broadening the
64 Bioinformatics Infrastructure to unicellular, animal and plant science" (FP7 GA 289452), for example,
65 concentrated on non-human genomes, applying human-genome-derived computational solutions to
66 non-human-genomics research questions [2]. This project involved the collection of a range of
67 biological problems – so-called '**test-cases**' – the computational solutions to some of which were
68 worked out in detail during '**hackathons**'.

69 A hackathon is a short (1-day to 1-week) event where stakeholders with diverse skills and backgrounds
70 gather to develop and implement solutions (usually in the form of software) to relevant problems. The
71 term hackathon is a composite of the words 'hack' (meaning exploratory programming) and
72 'marathon' (a common metaphor for events that are long and intensive). Hackathons are common in
73 informatics communities but still relatively new to the life sciences. In part, this may be because there

74 are still considerable communication gaps between life- and computational-science researchers.
75 Bioinformatics hackathons, or 'biohackathons' aim to address such gaps specifically by bringing IT
76 professionals (and interested amateurs) and life scientists together to communicate and exchange
77 ideas around practical research questions. They can be very effective, highly productive mechanisms
78 for interdisciplinary teams to work together either to solve well-defined problems or to accelerate
79 solution provision in a particular area. The short time normally available for (bio-) hackathons
80 generally allows for the design and implementation of prototype solutions; if the outputs are to be
81 useful, the developed code must have the potential to undergo subsequent development by
82 interested parties. Therefore, all results should be made available via open accessible platforms so
83 that further improvements can be made after the event has terminated.

84 The philosophy of the AllBio project was to solicit the needs of life scientists directly, in order to
85 identify interesting challenges. Around 60 such test-cases were collected via questionnaires and
86 interviews, of which 15 (encompassing unicellular organisms, plants, and farm animals) were deemed
87 solvable with adaptations to software or workflows originally designed for working with human-
88 genome data[3]. Eight were subsequently addressed in biohackathons [4,5]. A problem was
89 considered solvable when:

- 90 ● a generic question relating to the analysis of a unicellular, animal or plant genome had been
91 well defined,
- 92 ● a community of domain-expert bioscientists and bioinformaticians had been formed, and
- 93 ● scientific meetings (*in vivo* or *in silico*) had already taken place, and collaborations had begun.

94 The workflow for AllBio biohackathons involved the collection and selection of the test-cases,
95 preparation and organisation of the events, and finally - in case of success - publication of the results
96 (Fig 1).

97 **Figure 1. Identification of test cases.** AllBio workflow illustrating the fate of test-cases proposed by life scientists. After initial
98 interviews, test-cases were collected, and assessed for their tractability. The biohackathon teams comprised the proposer
99 (life scientist), a leader (bioinformatician), 'hackers' (programmers) and, usually, a local organiser. Where a tool or meta-tool

100 arose from the work, it was proposed for testing during a validation workshop. Ultimately, the team prepared an open source
101 tool, and published or otherwise disseminated the results.

102 During the AllBio project, a rigorous regime of evaluating past events allowed each biohackathon to
103 build on lessons learned from previous ones. This iterative process demonstrated that, for
104 biohackathons to be successful, the events must be well-prepared, long in advance; the biological
105 problems they set out to tackle must be tractable; they must have access to requisite computational
106 infrastructure, and allow sufficient time to complete the necessary tasks; and they must have efficient
107 leadership, an appropriate mix of skills/expertise, and effective communication strategies.
108 Biohackathons should be preceded by a preparatory phase to check feasibility and practicability (e.g.,
109 can the data actually be moved around and read); there should also be commitments afterwards to
110 finalise any tools (or other outputs), to test and validate them with end-users, and to disseminate the
111 results.

112 Based on the experience gained in AllBio, we present ten rules that we believe are crucial when
113 organising bioinformatics hackathons, or 'BioHackathons': these fall into four main categories - the
114 Problem, the Team, the BioHackathon and the Answer, which are described in detail below. There
115 will, of course, be other important considerations (funding, etc.), but we focus here on the
116 practicalities of organising successful biohackathons.

117 **The Ten Rules**

118 **The Problem**

119 **Rule 1: Understand the biological problem(s) and select the theme**

120 It might seem self-evident to state that a good starting point is to understand a problem before trying
121 to address it. But solving biological problems via hackathons requires a spectrum of understanding
122 that encompasses the biology of the problem (including *in vivo* aspects), the nature of the data
123 available, the nature of the computational requirements, the nature of the expected output(s), and
124 how all of these can be brought together to implement a viable solution. One of the keys to success is
125 that those responsible for implementing the technical solution(s) must appreciate, at least at some

126 level, the underlying biology. Ultimately, this requires some investment of time, in order to allow them
127 to begin to understand the language of those whose biological problems they are trying to solve. One
128 way to help achieve this, even for small events, might be to run a small cycle of webinars before the
129 event, in order to give participants more information about the theme. This is likely to facilitate team
130 building, and may also provide opportunities to come up with new ideas for possible approaches and
131 solutions.

132 **Rule 2: Ensure that the problem is tractable**

133 BioHackathons are driven by practical research questions, but not all biological problems are
134 amenable to solution by hackathons. An early step in setting up any such event should therefore be
135 to estimate whether the size of the problem is compatible with the hackathon format. For example,
136 while *de novo* software design is generally not the goal of -hackathons (design of new algorithms
137 tends to require more than just a few days), proof-of-concept implementations can fit the format
138 quite well. Ideally, therefore, the necessary software components must already exist, so that (bio-)
139 hackathon sessions can readily combine them into bespoke workflows. Ideally, workflows should not
140 contain any single point of failure.

141 Importantly, both the biological data-sets and the software components must be available without
142 restrictions.

143 **The Team**

144 **Rule 3: Put together the right team with carefully assigned roles**

145 Start building the team as soon as possible; ideally, aim to establish the core group two months prior
146 to the event. Think about life- and computational-science colleagues and students who have the
147 requisite skills and knowledge in the problem area. Generate a check-list with the minimal
148 requirements needed to ensure that the complete project can be implemented during the event; this
149 will form the basis for participant selection. If necessary, promote the biohackathon widely (*e.g.*, using
150 social media), providing as much information about the event as possible (including when, where,
151 what, how, fees (if needed) and registration forms). To engage biohackathon participants, some

152 incentives might be helpful: e.g., cooperation with university groups that might be willing to give credit
153 points for participation; or formulating problems whose solutions are suitable for academic
154 publication and crediting those participants as authors.

155 (Bio-)Hackathon teams are generally most effective when they comprise no more than eight to ten
156 participants. In general, they should include a proposer or 'biological problem owner' (typically a life
157 scientist) whose needs will drive the event; a leader (usually a bioinformatician); the 'hackers'
158 (bioinformaticians and computer scientists); and, ideally, an overall organiser/coordinator. Those with
159 computational skills should include at least one IT professional or bioinformatician, and programmers
160 with experience in scripting, workflow design, use of ontologies, evaluation of data quality, and so on.
161 These professionals must be able to communicate effectively with the leader and remain focused on
162 the primary objective.

163 The biohackathon leader is responsible for monitoring and guiding the workflow during the event. The
164 organiser must take responsibility for the overall coordination of the event, maintaining good
165 communication within the team (rule 4), orchestrating the validation (rule 9) and dissemination (rule
166 10) activities. The organiser must be local to the venue of the (bio-)hackathon, and will be responsible
167 for many mundane practical tasks: reserving the venue, testing bandwidth in the meeting room before
168 the actual hackathon, providing travel instructions, communication with the compute provider,
169 selecting the participants and dealing with subsistence/refreshment issues, etc. Several roles may be
170 assumed by one person, but it is vital that each partner knows his/her role, and that all roles are
171 maintained before, during and after the hackathon itself. To facilitate discussion and assignment of
172 tasks as the project progresses, we suggest adopting a convenient communication platform (*e.g.*,
173 **Trello** [6], **Slack** [7] or comparable platform [8,9,10]).

174 **Rule 4: Communicate effectively and establish the ground rules**

175 Communication – before, during and after hackathons – is key. The value of good communication, and
176 the impact of not getting it right, is hard to over-emphasise. Biohackathons include partners from
177 different disciplines, who tend to speak very different languages – if a biohackathon is to be maximally

178 productive, it is critical to take time, early on, to identify and resolve potential language barriers.
179 Frequent conversations prior to the biohackathon (in person if possible, or electronically if not), are
180 essential to begin to understand, define and refine the biological question, to identify and shape the
181 overall analytical approach, and thence to build 'ownership' of the tasks. As the technical partners
182 assimilate the nature of the biological problem, and the biological partners begin to appreciate the
183 nature of the technical challenges, the team's purpose, focus and cohesiveness will mature.

184 If multiple projects are being tackled in one biohackathon, ensure that all requirements have been
185 established beforehand, including the process of team-building, the time-frame available for each
186 problem (equal conditions for every team, so that each has the same relative chance of success), and
187 the rules for allowing participants to move between teams.

188 **Rule 5: Prepare the ground-work well in advance**

189 (Bio-)Hackathons are generally time-limited – good preparatory work is therefore essential. A crucial
190 part of the preparation is to test the necessary software and hardware prior to the event, in order to
191 obviate the occurrence of problems that could reduce the time available for hands-on work. Any heavy
192 computational tasks should be pre-computed to allow participants to hit the ground running with real
193 data. Biohackathon leaders must therefore fully understand all the components in advance, arrange
194 to have them tested in good time, and ensure that both software tools and hardware facilities are
195 adequate for the tasks at hand. For example, CPU-intensive tasks might require massive pre-
196 calculations and/or specialised equipment (such as all-against-all BLAST [11] computations on data-
197 sets with millions of sequences, or the assembly of very large genomes). Just as important is
198 verification of the quality of any data-sets to be used during the event, as poor-quality data-sets are
199 likely to jeopardise the success of (bio-) hackathon sessions. In order not to waste valuable time, any
200 task that can be tackled by a participant in isolation (without requiring the insight of the full team)
201 should be completed in advance. It is vital to test all software and hardware prior to the event. Work
202 with the hackers to establish the hardware requirements. Ensure that hardware
203 equipment/components can be provided or replaced temporarily, if need be.

204 Prepare a budget forecast for the event. The budget will be dedicated to the rental of premises, IT
205 requirements and subsistence. Gather options of suitable venues, and their prices. Look at the
206 premises and find out what the rental includes. Fix the premises for the scheduled date.

207 Decide the total amount you can spend on subsistence. We recommend creating a spreadsheet of all
208 costs. If you have no funds available, you will need to set a fee (which will ultimately be determined
209 by the number of participants, including lecturers, organisers, and so on). If you do have to set fees,
210 you should also be aware of the potential fiscal risks. Involve your administration in the process to
211 ensure that you do not run into trouble: they will know best how to treat fee income. If feasible, search
212 for potential sponsors – *e.g.*, companies with an interest in your BioHackathon theme.

213 We recommend creating a checklist for all tasks to be done before, during and after the event. Spread
214 responsibility between the organisers, but ensure that they do their job seriously. Discuss and agree
215 on the rules and procedures, and take care that they are followed strictly. Fig 2 collates the
216 organisational workflow for a complete biohackathon cycle, including the preparatory,
217 implementation and follow-up phase.

218 **The BioHackathon**

219 **Rule 6: Choose a convenient location**

220 (Bio-)Hackathons should take place at locations that are convenient for the registered number of
221 participants, and that can fulfil all scientific/computing and non-scientific (housing, food, *etc.*) needs.
222 University/national computing centres are likely to offer excellent computational facilities, but may
223 have restrictive opening hours. Hotels, on the other hand, while often very convenient in many
224 aspects, may overestimate the bandwidth they can provide, so this needs to be tested extensively
225 upfront.

226 Specific requirements to consider thus include:

- 227 ● location convenient for participants to reach (minimise travel time and cost),
- 228 ● short distance between accommodation and meeting venue (if the venue is not the hotel),

- 229 • venue technically well equipped (beamer, screen, *etc.*), with liberal opening hours (often,
230 much work is done outside normal working hours, and it is important to facilitate this),
- 231 • venue has sufficient and stable bandwidth,
- 232 • food and drink are either available at the venue or allowed to be brought in. Often, many
233 productive discussions occur informally over dinner, so arrangements that encourage the
234 participants to keep together while eating are strongly preferred.

235 **Rule 7: Ensure appropriate computer access**

236 All biohackathons are not equal: some will have greater computational requirements than others.
237 Some analyses might run efficiently on participants' own laptops; some might require access to large
238 clusters, supercomputers, dedicated hardware, or the cloud, which universities or national computer
239 centres may be willing to provide. Regardless, the prerequisites are i) fast internet connection at the
240 hackathon venue, and ii) possibility for remote login to the compute facilities before and after the
241 event, so that the groundwork can be prepared beforehand, and any remaining work can be
242 completed later. The local organiser should ensure (and check) that logins are available for all
243 participants, and ideally perform a test-run before the biohackathon. Similarly, if participants use their
244 own laptops, the requisite software should be installed prior to the event. It is recommended to create
245 a Virtual Machine to provide a common compute environment for participants. To gain an overview
246 of the software and hardware that will be needed during the biohackathon, we recommend gathering
247 information about technical requirements via the registration form. Share this information with the
248 hackers at the latest 10 days before the event.

249 **Rule 8: Ensure the duration is sufficient to obtain useful outputs**

250 (Bio-)Hackathons are short, intensive working sessions, typically spanning a few days. Several
251 considerations determine the duration of these events: the complexity of the workflow, how much
252 computer work is envisaged (and how much can be done in advance), the funds available, how much
253 time participants are able to commit, and whether writing documentation and/or article outlines are
254 also intended to be part of the exercise. The expected outputs must therefore be clearly defined early

255 on, and the duration of the event adjusted accordingly. It generally works well to organise hackathons
256 over a weekend, as this affords participants greater flexibility with their schedules.

257 To kick off the event, plan to run a series of short lectures to better inform participants about the
258 theme of the BioHackathon, and introduce its biological and computational components. Ensure the
259 availability of suitably qualified lecturers. Disseminate information about these lectures both to the
260 participants and to a broader audience at the latest two weeks before the hackathon. This may
261 stimulate greater interest in the event, and gain visibility within the community.

262 The lecture hall and work spaces might be at different locations. Ensure that you provide sufficient
263 and detailed information about where and when to go to each place. If there is not sufficient space to
264 comfortably accommodate additional participants in the lecture series, just focus on briefing the team.
265 This can also be done in the form of webinars before the event.

266 **The Answer**

267 **Rule 9: Validate the results**

268 BioHackathons aim to address particular biological problems. The events may focus on prototyping
269 ideas, or they may lead to the production of tools or meta-tools that will ultimately be made available
270 to the community. Prior to public release, 'validation' events should be organised, in which
271 participants are given opportunities to test the tool(s) with a variety of different data-sets. Even
272 though validation is normally done after hackathons, it should nevertheless be part of the initial
273 planning to ensure that validation data actually exist, and that the software set-up is sufficiently
274 generic to allow its use in validation. In an ideal case, most (if not all) of the original biohackathon
275 team should be present or (remotely) available during validation sessions.

276 **Rule 10: Disseminate the results**

277 Peer-reviewed publications are still the main vehicles for disseminating scientific results, and reusable
278 outputs from biohackathons are a good stimulus for article publication. Public availability of all
279 workflows must also be part of the dissemination strategy. Workflows should therefore be properly

280 documented and licensed, and inputs and outputs should be appropriately described. Ideally,
281 alongside any publicly accessible documentation or article, small data-sets that can be used by the
282 workflows should also be included. Optionally, Virtual Machine images to run workflows might also
283 be provided. Results should be made available through open accessible platforms (e.g. *seek* [12],
284 *OpenAIRE*, *Zenodo* [13, 14]) that can guarantee longevity, as good workflows that answer biological
285 questions often remain valuable for several years.

286 **Figure 2: Workflow.** The scheme demonstrates an optimal workflow for biohackathons, including the preparatory,
287 implementation and follow-up phase for a complete cycle. Each phase is subdivided into different consecutive steps: in
288 particular, the preparatory phase comprises a broad spectrum of tasks, including the selection of challenges, recruiting of
289 participants, organisation of the venue and technical set-up, as well as creation of webinars to prepare participants for the
290 event.

291 **Potential pitfalls**

292 The experience of the AllBio biohackathons provided an inside view of potential pitfalls that might
293 limit the success of such events. A primary challenge is careful selection of appropriate problems - not
294 all are suitable for inclusion in a BioHackathon. It requires expert knowledge from both the biology
295 and bioinformatics fields, to evaluate the challenges and avoid frustration for the participants.

296 A very specific function that biohackathons can perform is enabling interdisciplinary collaboration
297 between the participants from the different expert fields.. Sufficient time needs to be dedicated to
298 training participants, and finding a common language for discussing the challenges and developing
299 efficient solutions.

300 Other more practical aspects may limit the success of events: e.g., some early AllBio biohackathons
301 struggled to deliver concrete outputs because:

- 302 ● their teams were too small (≤ 5 people);
- 303 ● the team had no real leadership;
- 304 ● the data-sets on which they were obliged to work were too large to be processed fruitfully
305 within the given time-frame;

- 306 • the opening hours of computing centres limited the time available for productive work;
307 • the distance between hackathon venues and participants' hotels posed time- and cost
308 constraints.

309 A barrier to success may also occur if the meeting organiser/leader is no longer available after the
310 event; the validation and follow-up phase is essential for summarising the results, and ensuring the
311 quality of solutions that have been developed. Moreover, publication of the results, whether via a
312 journal article or upload to a repository, needs to be completed after the biohackathon. Costs
313 associated with the dissemination of results need to be considered in the overall budget plan.

314 **Conclusion**

315 Biohackathons were powerful tools in the AllBio project for articulating and solving problems in the
316 scientific community [3]. They highlighted the need to take into account the different disciplinary
317 backgrounds of all participants, and hence the vital role of the preparatory phase for ensuring the
318 success of events. They also provided excellent opportunities, especially for young researchers, to
319 learn new skills at the interface between disciplines, to participate in the advancement of their field
320 of research, and to gain unique hands-on training with real challenges.

321 Some of the rules listed here may seem obvious, trivial, or even superfluous; nevertheless, all proved
322 crucial in real-life scenarios. The ten rules provide practical guidelines for future biohackathon
323 organisers, including preparations before, during and after the event itself.

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330

331 **References**

- 332 [1] The Earth BioGenome Project (EBP) aims to sequence, catalog and characterize the genomes of
333 all of Earth’s eukaryotic biodiversity over a period of ten years. Available from:
334 <https://www.earthbiogenome.org/>
- 335 [2] Broadening the Bioinformatics Infrastructure to unicellular, animal, and plant science. Available
336 from: <http://www.allbioinformatics.eu/doku.php/>
337 <https://cordis.europa.eu/project/rcn/100520/factsheet/en>
- 338 [3] Broadening the bioinformatics infrastructure to unicellular, animal, and plant science D5.3 - Final
339 summary report on solved test cases. Available from: <https://doi.org/10.5281/zenodo.3525052>
- 340 [4] Steinhilber D, Rodriguez A, Vlachakis D, Virgo G, Maksimov V, Kristell C, et al. (2014) Silencing
341 Motifs in the Clr2 Protein from Fission Yeast, *Schizosaccharomyces pombe*. PLoS ONE 9(1): e86948.
342 <https://doi.org/10.1371/journal.pone.0086948>
- 343 [5] Gomez-Cabrero et al.: Data integration in the era of omics: current and future challenges. BMC
344 Systems Biology 20148(Suppl 2):11 doi:10.1186/1752-0509-8-S2-11
- 345 [6] Online tool of boards, lists, and cards to organise and prioritise projects in a fun, flexible, and
346 rewarding way. Available from: <https://trello.com/>
- 347 [7] Web-based instant messaging service Available from: <https://slack.com/>
- 348 [8] OwnCloud is an open source software for cloud-based collaboration platforms. Available from:
349 <https://owncloud.org/>
- 350 [9] Open source software for cloud-based collaboration platforms. Available from:
351 <https://drive.google.com>
- 352 [10] Dropbox is a modern workspace designed to reduce busywork-so you can focus on the things
353 that matter. Available from: <https://www.dropbox.com>
- 354 [11] Basic Local Alignment Search Tool. Available from: <https://blast.ncbi.nlm.nih.gov/Blast.cgi>
- 355 [12] The FAIRDOM Platform uses a stack of software platforms to provide a “Project Commons” –
356 that is, a shared place where projects can organise their own data, models, protocols, workflows in
357 their own managed space. Available from: <https://fair-dom.org/platform/>

358 [13] Repository to deposit research products of any type (publication, data, software, other)

359 Available from: <https://explore.openaire.eu/participate/deposit-publications>

360 [14] Online storage service used for scientific data sets, science-related software, publications,

361 reports, presentations, videos, etc. Available from: <https://zenodo.org/>